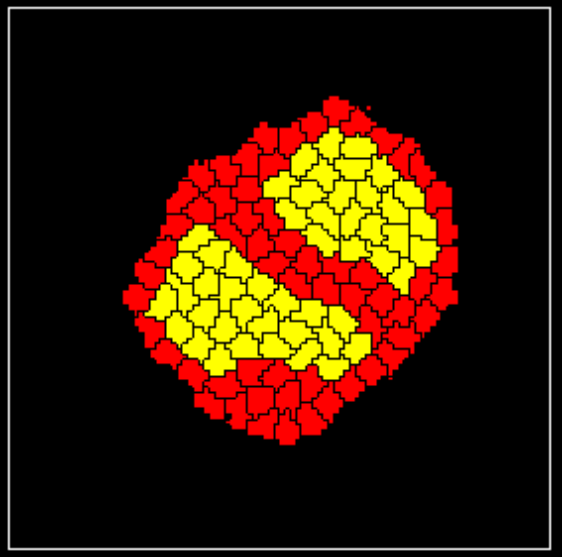
A guide to the cellular Potts model

Computational Biology Working Group Seminar
University College London
4. September, 2013



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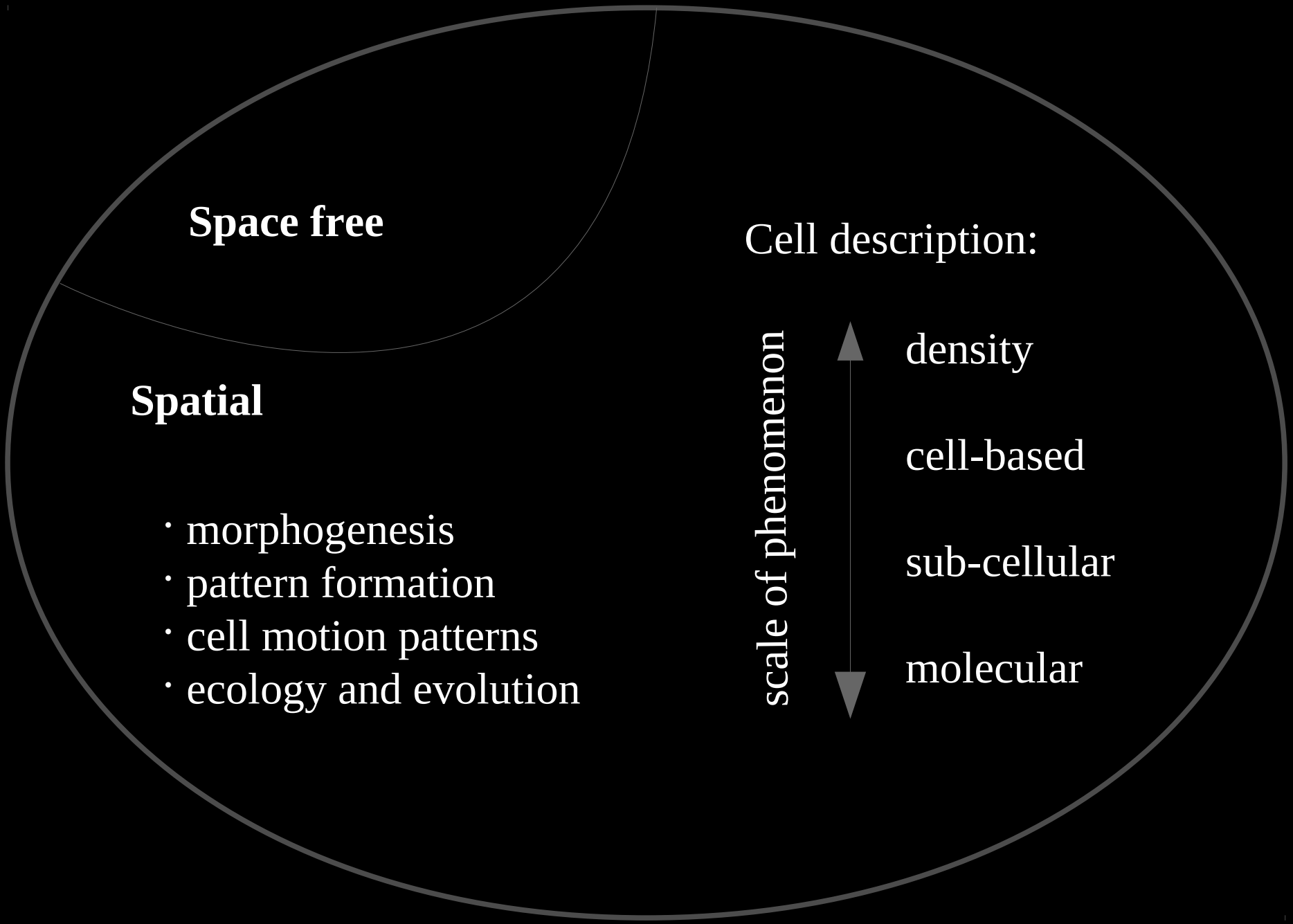
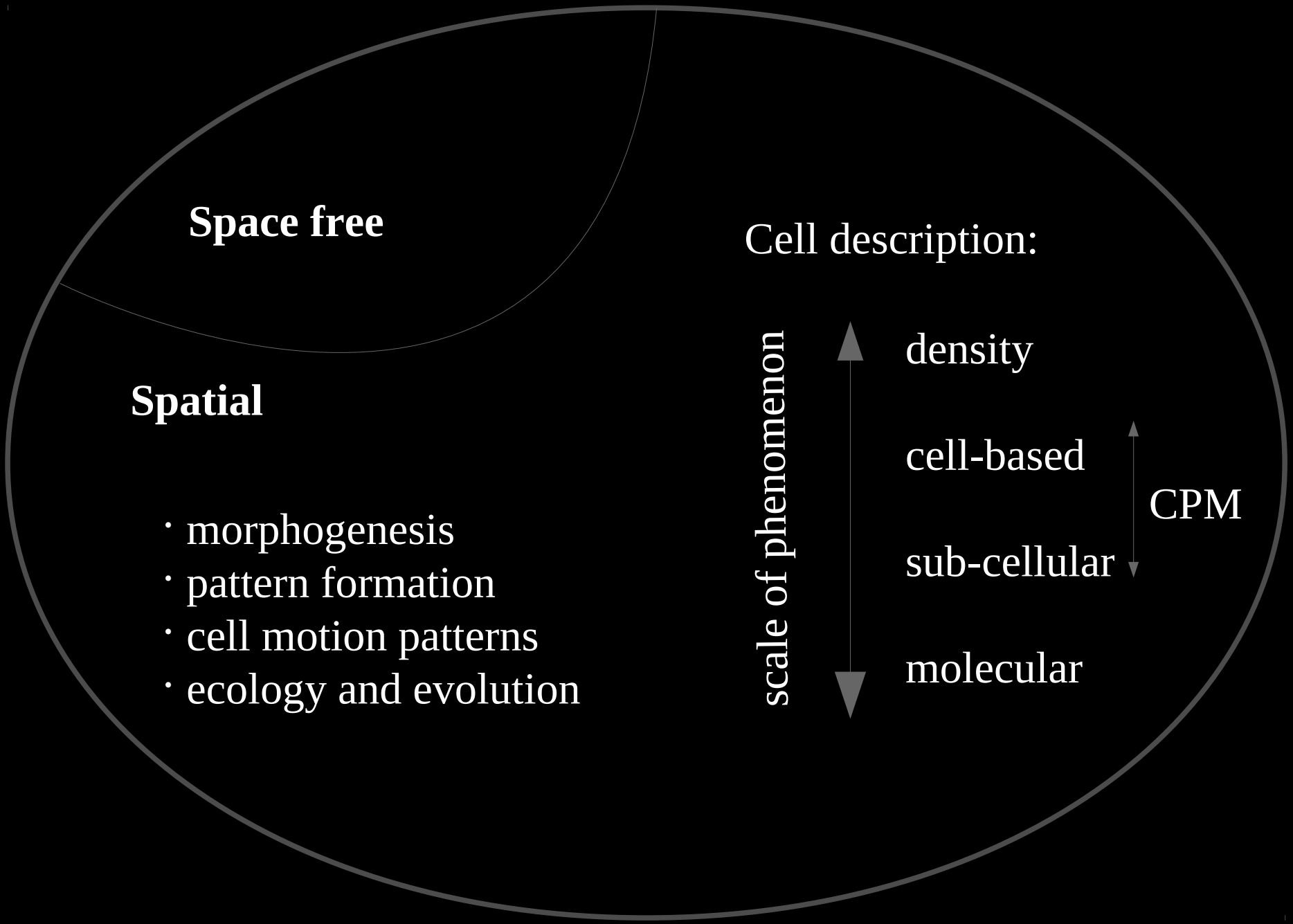
Models in biology

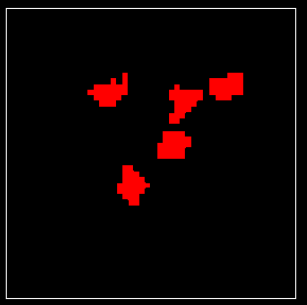


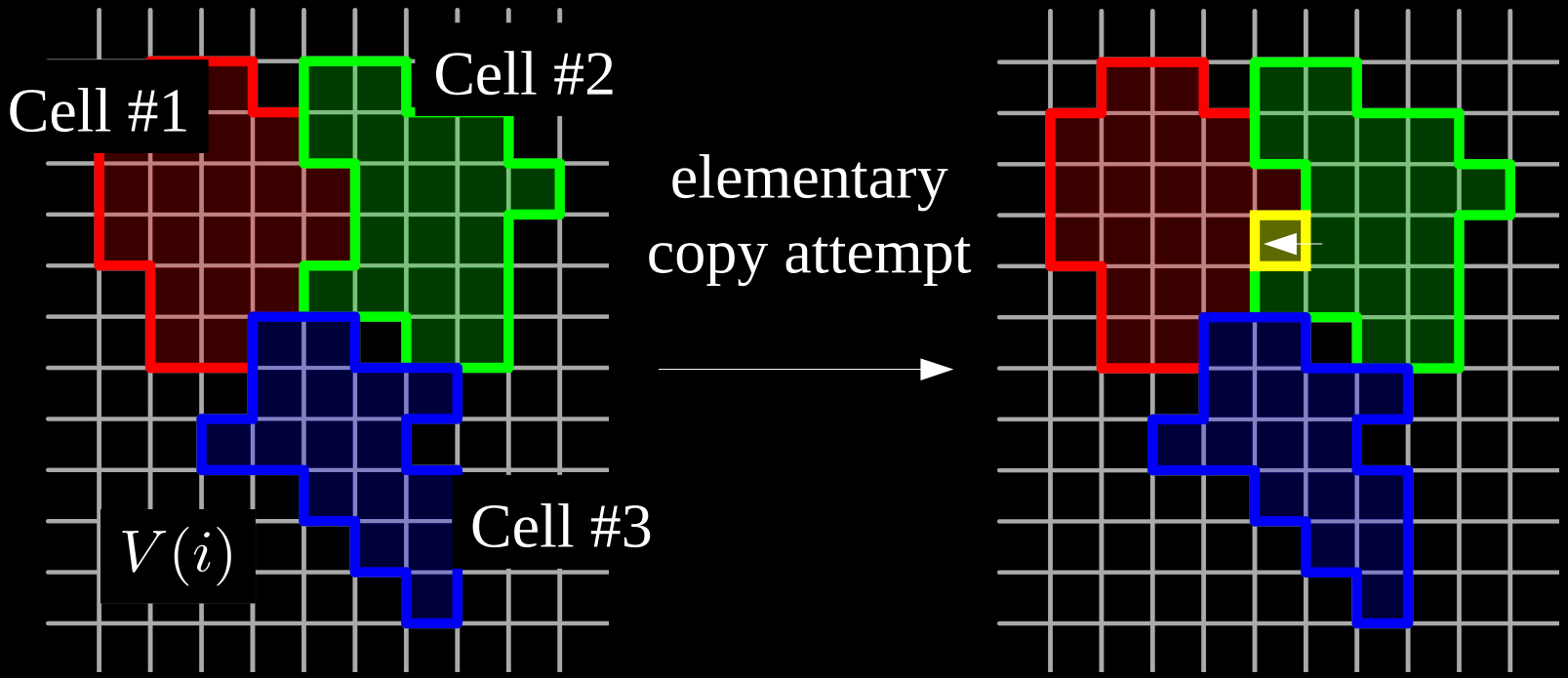
Models in biology



The cellular Potts model

Features:
- cells as fluid droplets (~ constant volume, $V_T(i)$)
- adhesion as surface tension
- stochastic, amoeboid cell motion





N elementary attempts is a time step: Monte Carlo step (MCS)

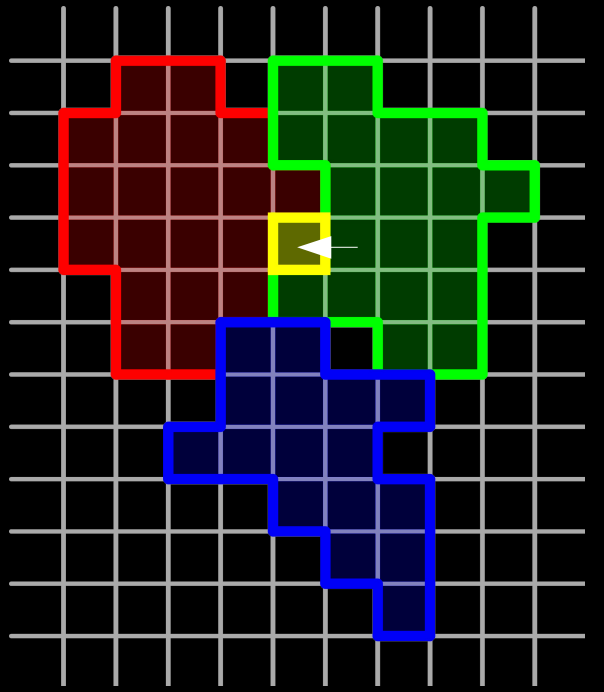
Model dynamics

Acceptance probability:

$$p = e^{\frac{\Delta H}{T}}$$

change in “Hamiltonian” (~ cost) function

motility (temperature) parameter



Hamiltonian function:

Volume term

Adhesion term

$$H = \lambda_v \sum_i (V(i) - V_{\mathrm{t}}(i))^2 + \sum_{<i,j>} J(i,j)(1 - \delta_{i,j})$$

“lambda” volume

target volume

adhesion (or J) matrix

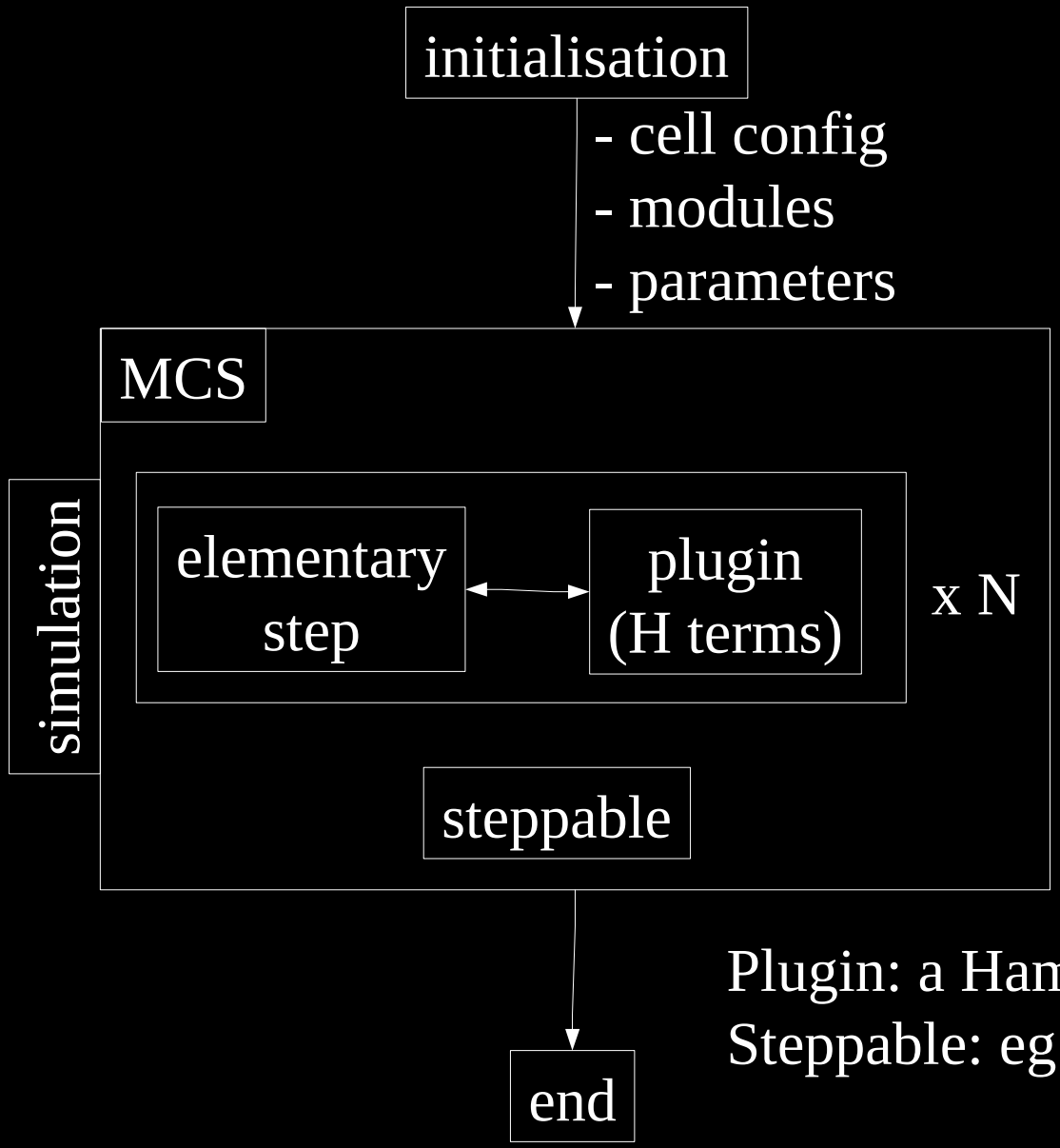
Kronecker's delta

Two CPM Implementations

Open source
Compatible with the 3 mayor platforms (Win, Mac, Linux)

CompuCell3D	**Tissue Simulation Toolkit**
Executable available Community backed (forum, help service, workshops)	Source code only Support and development is small (missing?)
2 levels of interaction (novice-py and advanced-C++)	Intermediate difficulty, simpler code
Main dependencies: VTK, python	Main dependency: Qt

CompuCell3D



Model definition:
- initial cell configuration
- modules
- parameters

Modular code structure:
- kernel + modules

Modules:
- “plugins” (per E.S.)
- “steppables” (per MCS)

Defined in xml and/or python

Plugin: a Hamiltonian term (eg: volume, adhesion)
Steppable: eg: cell division, cell growth

New modules in python or C++

→ www.CompuCell3D.org

CompuCell3D

2 main interfaces:

- compucell3d: simulation runs
- twedit++ : customised editor

Examples:

- Cell sorting (xml only, predefined modules)
- Feeder example (sorting + one type feeds the other)
- Creating a sorting model using Twedit++

Tissue Simulation Toolkit

Model defined by the whole code (not modular)
Code structure:

- one directory with a handful of C++ source files
- “plugins” in **ca.cpp** **(**function DeltaH)
- “steppables” in **ca.cpp** (function AmoebaeMove)
- cell properties in **cell.h** and **cell.cpp**
- everything with PDE's goes to **pde.h** / **pde.cpp**
- main scripts: engulfment / pushing / sorting / tumor / vessel

Parameters read from separate parameter file

Exmaples:

- sorting (sorting.par)
- checked sorting (checked.par)
- persistent cells (spp.par)
- persistent, adherent (viscous) cells (spp2.par)

Available from: http://sourceforge.net/projects/tst/

Summary

- CPM: stochastic, cell-based, multi-particle model
- Useful for modelling:
    morphogenesis, pattern formation, cell migration, etc.
- Open source implementations here presented:
    - CompuCell3D:
        - 2D / 3D
        - easy to use interface (python and C++)
        - continuously developing, active support
    - Tissue Simulation Toolkit:
        - 2D only
        - C++ only
        - can serve as a sand-box for more complex features

- The CPM can also be re-implemented using other tools (eg: MatLab)

Thank you for your attention

CompuCell3D:

http://www.compucell3d.org/

Development directed by:

James Glazier, Indiana University

http://www.indiana.edu/~bioc/jglazier/

Tissue Simulation Toolkit:

http://sourceforge.net/projects/tst/

Development directed by:

Roeland Merks, CWI (Amsterdam)

http://biomodel.project.cwi.nl/

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